

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/623,567A
Source: IFWO
Date Processed by STIC: 2-9-05

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 02/09/2005

PATENT APPLICATION: US/10/623,567A

TIME: 10:27:09

Input Set : A:\012679-093.txt

Output Set: N:\CRF4\02092005\J623567A.raw

```

4 <110> APPLICANT: Kim, Sunghoon
6 <120> TITLE OF INVENTION: Method for Stimulating Wound Healing
9 <130> FILE REFERENCE: 012679-093
11 <140> CURRENT APPLICATION NUMBER: US 10/623,567A
12 <141> CURRENT FILING DATE: 2003-07-22
14 <150> PRIOR APPLICATION NUMBER: KR 10-2002-42858
15 <151> PRIOR FILING DATE: 2002-07-22
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 312
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
27 Met Ala Asn Asn Asp Ala Val Leu Lys Arg Leu Glu Gln Lys Gly Ala
28 1 5 10 15
29 Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ser Leu Leu
30 20 25 30
31 Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu
32 35 40 45
33 Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln
34 50 55 60
35 Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe
36 65 70 75 80
37 Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val
38 85 90 95
39 Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln
40 100 105 110
41 Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu
42 115 120 125
43 Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
44 130 135 140
45 Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly
46 145 150 155 160
47 Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val
48 165 170 175
49 Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly
50 180 185 190
51 Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile
52 195 200 205
53 Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln
54 210 215 220
55 Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala

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```

56 225          230          235          240
57 Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe
58          245          250          255
59 Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu
60          260          265          270
61 Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
62          275          280          285
63 Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
64          290          295          300
65 Thr Met Ser Asn Ser Gly Ile Lys
66 305          310
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 108
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: probe for Southern blot
77 <400> SEQUENCE: 2
78 tgaatgaact gcaggacgag gcagcgcggc tatggtggct ggccacgacg ggcgttcctt 60
79 gcgcagctgt gctcgacgtt gtcactgaag cgggaaggac tggctgct 108
81 <210> SEQ ID NO: 3
82 <211> LENGTH: 1226
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: probe for Southern blot
W--> 89 <221> NAME/KEY: misc_feature
90 <222> LOCATION: 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67,
91          68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 646, 647,
92          648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659,
93          660, 661, 662, 663, 1212, 1213, 1214, 1215, 1216, 1217
94 <223> OTHER INFORMATION: n = A,T,C or G
W--> 96 <221> misc_feature
97 <222> LOCATION: 1218, 1219, 1220, 1221
98 <223> OTHER INFORMATION: n = A,T,C or G
W--> 100 <400> 3
W--> 101 aagcttcgac catatgggag agctcccaac gcgttgatg catagcttga gtnnnnnnnn 60
102 nnnnnnnnnn nnnnnnnnng aattcaataa ggagactttt taaaaagata tttttatctt 120
103 aatgtgtgtg tgctgcatt tgtgtgatg caccattgag tgcataccta gagcctgcag 180
104 aggctagaag aggggttcaa cctggaactg aggctacagg tgggtgttga gtatccacat 240
105 agatgctcgg aattaaacct gggttctcca gtcccaagga gactaaatat tttcaaagta 300
106 agcctgcact ttgtactaca gtaaaataaa accactgtgg agtgactaat ataaaatagt 360
107 aagatgagct ctagattaac aggcaaaagt ttaagttttc agtattgtta aagtagcacc 420
108 atctccctaa agagaacctat atttattttc cttccagtct tctgtgtttc cctcttttgt 480
109 ttgaaagttt agtgagtgct tattttctct actgtgaaca caacatgaga caaactcagg 540
110 gattgtaaga gatcatggac ataaattact tttaggaacc tggcactcaa atgaaaatta 600
111 attagtgaac agttggcatg gcattttatt attaaccctg ggtggnnnnn nnnnnnnnnn 660
112 nnntaaactg cgtggtgatg atttgtgatt gcaagaagac atagatatga agctctgaac 720
113 aacagtgtcc aggcaacatg tgaagaaaag gccctatgga ggggcaggag agcagggtgag 780

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```

114 agcatcctaa tagaaattca gacagtgaag caagaagttg ttcacacagc ccacacagcc 840
115 tgttaagtgt tcttcactta aggtttgttg actgtaacca ctttttctaa agaaaacatt 900
116 aagaaaaaca taggtgtctg ttcgcttctt atttgtgtgt gtgattaaaa cgctgaccaa 960
117 aagcaacttg gctgaggagc cgtttttgta tttctccgtt taggtagcaa tgaagttgga 1020
118 gcaggaggaa ggggtgcttac aggctagctc tctgtctctc cttgagcaag cattcttggtg 1080
119 gtagctcagg actccctgca cagtgcacac ccacgtgctt cttcaggggg acttcaaact 1140
120 actgtacacc ctttcttctt gtcgaccata tgggagagct cccaacgcgt tggatgcata 1200
121 gcttgagtat tnnnnnnnnn nagctt 1226
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 30
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: IF3 primer for PCR
131 <400> SEQUENCE: 4
132 gaggacaatg tgctccataa acactcactg 30
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 27
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: IR3 primer for PCR
142 <400> SEQUENCE: 5
143 cgttacttaa gctagcttgc cacctac 27
145 <210> SEQ ID NO: 6
146 <211> LENGTH: 31
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: pKOF2 primer for PCR
153 <400> SEQUENCE: 6
154 tgacatgggt gccagagaag gttctcaagg a 31
156 <210> SEQ ID NO: 7
157 <211> LENGTH: 838
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: p43-specific probe for Northern blot
164 <400> SEQUENCE: 7
165 ggtcaccgct tcatgtttct ctgccgattc tggggaaaga tggcaacgaa tgatgctggt 60
166 ctgaagaggc tggagcagaa ggggtgcagag gcggatcaga tcatcgaata tctcaagcag 120
167 cagggtgtct ttcttaagga gaaagcaatt ttgcaggcaa caatgagaga agaaaagaaa 180
168 cttcgagttg aaaatgctaa actgaaaaaa gaaatagaag agctaaagca agagctgatt 240
169 ctggcagaaa ttcataacgg agtgaggcaa gtgcgtgttc gattgagtac tccactgcag 300
170 acgaactgta ctgcttctga aagtgtggtg cagtctccat cagtagcaac caccgcctct 360
171 cctgctacaa aagagcagat caaagcgagg gaagaaaaga aggtgaaaga gaagactgaa 420
172 aagaaaggag agaaaaagga gaagcagcag tcggcagcag caagtactga ctccaagcct 480
173 atcgacgcat cgcgtctgga tcttcgaatt ggttgatttg ttactgcaa gaagcaccct 540
174 gatgcagatt cactgtatgt ggaggaagta gatgtgggag aagcagcccc gcgcacgggtc 600

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```
175 gtcagcgggc tggatgaatca tggtcctcta gaacagatgc aaaatcgtat ggtgggtttta 660
176 ctctgtaatc tgaagcctgc aaagatgcgg ggagttctgt ctcaagccat ggtgatgtgt 720
177 gccagttcac cagagaaagt ggagattctg gcccctccca acgggtccgt tcctggggac 780
178 agaattactt ttgatgcttt tcctggagag cctgacaagg agctaaaccc taagaaga 838
```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/623,567A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72
Seq#:3; N Pos. 73, 74, 75, 76, 77, 78, 79, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655
Seq#:3; N Pos. 656, 657, 658, 659, 660, 661, 662, 663, 1212, 1213, 1214, 1215, 1216
Seq#:3; N Pos. 1217, 1218, 1219, 1220, 1221

VERIFICATION SUMMARY

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L:89 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:96 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3